

Figure 1

M K H L W F F L L L V A A P R
 GAC ATG AAA CAC CTG TGG TTC TTC CTC CTC CTG GTG GCA GCC CCC AGA
 +1 10
 W V L S Q V Q L Q E A G P G L V
 TGG GTC TTG TCC CAG GTG CAG CTG CAG GAG GCG GGC CCA GGA CTG GTG
 20
 K P S E T L S L T C S V S G G S
 AAG CCT TCG GAG ACC CTG TCC CTC ACC TGC AGT GTC TCT GGT GGC TCC
 30 40
 I S G D Y Y W F W I R Q S P G K
 ATC AGC GGT GAC TAT TAT TGG TTC TGG ATC CGC CAG TCC CCA GGG AAG
 50 60
 G L E W I G Y I Y G S G G G T N
 GGA CTG GAG TGG ATC GGC TAC ATC TAT GGC AGT GGT GGG GGC ACC AAT
 70
 Y N P S L N N R V S I S I D T S
 TAC AAT CCC TCC CTC AAC AAT CGA GTC TCC ATT TCA ATA GAC ACG TCC
 80 90
 K N L F S L K L R S V T A A D T
 AAG AAC CTC TTC TCC CTG AAA CTG AGG TCT GTG ACC GCC GCG GAC ACG
 100
 A V Y Y C A S N I L K Y L H W L
 GCC GTC TAT TAC TGT GCG AGT AAT ATA TTG AAA TAT CTT CAC TGG TTA
 110 120
 L Y W G Q G V L V T S S
 TTA TAC TGG GGC CAG GGA GTC CTG GTC ACC GTC TCC

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[illegible][illegible]

Frame 1	Met	Ala	Trp	Ala	Leu	Leu	Leu	Leu	Gly	Leu	Leu	Ala	His	Phe	Thr	Asp	Ser	Ala	Ala	
ATG	GCC	TGG	GCT	CTG	CTG	CTC	CTC	GGC	CTC	CTT	GCT	CAC	TTT	ACA	GAC	TCT	GCG	GCC		
	9			18				27				36			45			54		
Ser	Tyr	Glu	Leu	Ser	Gln	Pro	Arg	Ser	Val	Ser	Val	Ser	Pro	Gly	Gln	Thr	Ala	Gly	Phe	Thr
TCC	TAT	GAG	TTG	AGT	CAG	CCT	CGC	TCA	GTG	TCC	GTG	TCC	CCA	GGA	CAG	ACG	GCC	GGG	TTC	ACC
	66			75			84		93				102			111			120	
Cys	Gly	Gly	Asp	Asn	Val	Gly	Arg	Lys	Ser	Val	Gln	Trp	Tyr	Gln	Gln	Lys	Pro	Pro	Gln	Ala
TGT	GGG	GGA	GAC	AAC	GTT	GGA	AGG	AAA	AGT	GTA	CAG	TGG	TAC	CAG	CAG	AAG	CCA	CCG	CAG	GCC
	129			138			147		156				165			174			183	
Pro	Val	Leu	Val	Ile	Tyr	Ala	Asp	Ser	Glu	Arg	Pro	Ser	Gly	Ile	Pro	Ala	Arg	Phe	Ser	Gly
CCT	GTG	CTG	GTC	ATC	TAT	GCT	GAC	AGC	GAA	CGG	CCC	TCA	GGG	ATC	CCT	GCG	CGA	TTC	TCT	GGC
	192			201			210		219				228			237			246	
Ser	Asn	Ser	Gly	Asn	Thr	Ala	Thr	Leu	Thr	Ile	Ser	Gly	Val	Glu	Ala	Gly	Asp	Glu	Ala	Asp
TCC	AAC	TCA	GGG	AAC	ACC	GCC	ACC	CTG	ACC	ATC	AGC	GGG	GTC	GAG	GCC	GGG	GAT	GAG	GCT	GAC
	255			264			273		282				291			300			309	
Tyr	Tyr	Cys	Gln	Val	Trp	Asp	Ser	Thr	Ala	Asp	His	Trp	Val	Phe	Gly	Gly	Gly	Thr	Arg	Leu
TAT	TAC	TGT	CAG	GTG	TGG	GAC	AGT	ACT	GCT	GAT	CAT	TGG	GTC	TTC	GGC	GGA	GGG	ACC	CGG	CTG
	318			327			336		345				354			363			372	
Thr	Val	Leu	Gly	Gln	Pro	Lys	Ala	Ala	Pro	Ser	Val	Thr	Leu	Phe	Pro	Pro	Ser	Ser	Glu	Glu
ACC	GTC	CTA	GGT	CAG	CCC	AAG	GCT	GCC	CCC	TCG	GTC	ACT	CTG	TTC	CCG	CCC	TCC	TCT	GAG	GAG
	381			390			399		408				417			426			435	
Leu	Gln	Ala	Asn	Lys	Ala	Thr	Leu	Val	Cys	Leu	Ile	Ser	Asp	Phe	Tyr	Pro	Gly	Ala	Val	Thr
CTT	CAA	GCC	AAC	AAG	GCC	ACA	CTG	GTG	TGT	CTC	ATA	AGT	GAC	TTC	TAC	CCG	GGA	GCC	GTG	ACA
	444			453			462		471				480			489			498	
Val	Ala	Trp	Lys	Ala	Asp	Ser	Ser	Pro	Val	Lys	Ala	Gly	Val	Glu	Thr	Thr	Thr	Pro	Ser	Lys
GTG	GCC	TGG	AAG	GCA	GAT	AGC	AGC	CCC	GTC	AAG	GCG	GGA	GTG	GAG	ACC	ACC	ACA	CCC	TCC	AAA
	507			516			525		534				543			552				

4 / 32
Figure 4

Frame 1 Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp Val Leu Ser
ATG AAA CAC CTG TGG TTC TTC CTC CTC CTG GTG GCA GCC CCC AGA TGG GTC TTG TCC
9 18 27 36 45 54

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr
CAG GTG CAG CTG CAG GAG TCG GGC CCA GGA CTG GTG AAG CCT TCG GAG ACC CTG TCC CTC ACC
66 75 84 93 102 111 120

Cys Ser Val Ser Gly Gly Ser Ile Ser Gly Asp Tyr Tyr Trp Phe Trp Ile Arg Gln Ser Pro
TGC AGT GTC TCT GGT GGC TCC ATC AGC GGT GAC TAT TAT TGG TTC TGG ATC CGC CAG TCC CCA
129 138 147 156 165 174 183

Gly Lys Gly Leu Glu Trp Ile Gly Tyr Ile Tyr Gly Ser Gly Gly Gly Thr Asn Tyr Asn Pro
GGG AAG GGA CTG GAG TGG ATC GGC TAC ATC TAT GGC AGT GGT GGG GGC ACC AAT TAC AAT CCC
192 201 210 219 228 237 246

Ser Leu Asn Asn Arg Val Ser Ile Ser Ile Asp Thr Ser Lys Asn Leu Phe Ser Leu Lys Leu
TCC CTC AAC AAT CGA GTC TCC ATT TCA ATA GAC ACG TCC AAG AAC CTC TTC TCC CTG AAA CTG
255 264 273 282 291 300 309

Arg Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Ser Asn Ile Leu Lys Tyr Leu
AGG TCT GTG ACC GCC GCG GAC ACG GCC GTC TAT TAC TGT GCG AGT AAT ATA TTG AAA TAT CTT
318 327 336 345 354 363 372

His Trp Leu Leu Tyr Trp Gly Gln Gly Val Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly
CAC TGG TTA TTA TAC TGG GGC CAG GGA GTC CTG GTC ACC GTC TCC TCA GCT AGC ACC AAG GGC
381 390 399 408 417 426 435

Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly
CCA TCC GTC TTC CCC CTG GCG CCC TGC TCC AGG AGC ACC TCC GAG AGC ACA GCC GCC CTG GGC
444 453 462 471 480 489 498

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr
TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG TCG TGG AAC TCA GGC GCC CTG ACC
507 516 525 534 543 552 561

Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val
AGC GGC GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA GGA CTC TAC TCC CTC AGC AGC GTG
570 579 588 597 606 615 624

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro
GTG ACC GTG CCC TCC AGC AGC TTG GGC ACG AAG ACC TAC ACC TGC AAC GTA GAT CAC AAG CCC
633 642 651 660 669 678 687

Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro

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1. The first part of the report, which is the most important, is the introduction. This part should be written in a clear and concise manner, and should provide a brief overview of the project and its objectives.

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Frame 1	Met	Lys	His	Leu	Trp	Phe	Phe	Leu	Leu	Val	Ala	Ala	Ala	Pro	Arg	Trp	Val	Leu	Ser
	ATG	AAA	CAC	CTG	TGG	TTC	TTC	CTC	CTC	CTG	GTG	GCA	GCC	CCC	AGA	TGG	GTC	TTG	TCC
			9			18			27			36			45			54	
Gln Val	Gln	Leu	Gln	Glu	Ser	Gly	Pro	Gly	Leu	Val	Lys	Pro	Ser	Glu	Thr	Leu	Ser	Leu	Thr
CAG GTG	CAG	CTG	CAG	GAG	TGC	GGC	CCA	GGA	CTG	GTG	AAG	CCT	TCG	GAG	ACC	CTG	TCC	CTC	ACC
	66			75			84			93			102			111			120
Cys Ser	Val	Ser	Gly	Gly	Ser	Ile	Ser	Gly	Asp	Tyr	Tyr	Trp	Phe	Trp	Ile	Arg	Gln	Ser	Pro
TGC AGT	GTC	TCT	GGT	GGC	TCC	ATC	AGC	GGT	GAC	TAT	TAT	TGG	TTC	TGG	ATC	CGC	CAG	TCC	CCA
	129			138			147			156			165			174			183
Gly Lys	Gly	Leu	Glu	Trp	Ile	Gly	Tyr	Ile	Tyr	Gly	Ser	Gly	Gly	Gly	Thr	Asn	Tyr	Asn	Pro
GGG AAG	GGA	CTG	GAG	TGG	ATC	GGC	TAC	ATC	TAT	GGC	AGT	GGT	GGG	GGC	ACC	AAT	TAC	AAT	CCC
	192			201			210			219			228			237			246
Ser Leu	Asn	Asn	Arg	Val	Ser	Ile	Ser	Ile	Asp	Thr	Ser	Lys	Asn	Leu	Phe	Ser	Leu	Lys	Leu
TCC CTC	AAC	AAT	CGA	GTC	TCC	ATT	TCA	ATA	GAC	ACG	TCC	AAG	AAC	CTC	TTC	TCC	CTG	AAA	CTG
	255			264			273			282			291			300			309
Arg Ser	Val	Thr	Ala	Ala	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Ser	Asn	Ile	Leu	Lys	Tyr	Leu
AGG TCT	GTG	ACC	GCC	GCG	GAC	ACG	GCC	GTC	TAT	TAC	TGT	GCG	AGT	AAT	ATA	TTG	AAA	TAT	CTT
	318			327			336			345			354			363			372
His Trp	Leu	Leu	Tyr	Trp	Gly	Gln	Gly	Val	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly
CAC TGG	TTA	TTA	TAC	TGG	GGC	CAG	GGA	GTC	CTG	GTC	ACC	GTC	TCC	TCA	GCT	AGC	ACC	AAG	GGG
	381			390			399			408			417			426			435
Pro Ser	Val	Phe	Pro	Leu	Ala	Pro	Cys	Ser	Arg	Ser	Thr	Ser	Glu	Ser	Thr	Ala	Ala	Leu	Gly
CCA TCC	GTC	TTC	CCC	CTG	GCG	CCC	TGC	TCC	AGG	AGC	ACC	TCC	GAG	AGC	ACA	GCC	GCC	CTG	GGC
	444			453			462			471			480			489			498
Cys Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr
TGC CTG	GTC	AAG	GAC	TAC	TTC	CCC	GAA	CCG	GTG	ACG	GTG	TCG	TGG	AAC	TCA	GGC	GCC	CTG	ACC
	507			516			525			534			543			552			561
Ser Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val
AGC GGC	GTG	CAC	ACC	TTC	CCG	GCT	GTC	CTA	CAG	TCC	TCA	GGA	CTC	TAC	TCC	CTC	AGC	AGC	GTG
	570			579			588			597			606			615			624
Val Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Lys	Thr	Tyr	Thr	Cys	Asn	Val	Asp	His	Lys	Pro
GTG ACC	GTG	CCC	TCC	AGC	AGC	TTG	GGC	ACG	AAG	ACC	TAC	ACC	TGC	AAC	GTA	GAT	CAC	AAG	CCC
	633	</																	

7 / 32
Figure 5 (Continued)

AGC	AAC	ACC	AAG	GTG	GAC	AAG	AGA	GTT	GAG	TCC	AAA	TAT	GGT	CCC	CCA	TGC	CCA	TGC	CCA
696					705			714			723			732			741		750
Ala	Pro	Glu	Phe	Glu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr
GCA	CCT	GAG	TTC	GAG	GGG	GGA	CCA	TCA	GTC	TTC	CTG	TTC	CCC	CCA	AAA	CCC	AAG	GAC	ACT
		759			768			777			786			795			804		813
Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	Gln	Glu	Asp	Pro
ATG	ATC	TCC	CGG	ACC	CCT	GAG	GTC	ACG	TGC	GTG	GTG	GTG	GAC	GTG	AGC	CAG	GAA	GAC	CCC
		822			831			840			849			858			867		876
Val	Gln	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg
GTC	CAG	TTC	AAC	TGG	TAC	GTG	GAT	GGC	GTG	GAG	GTG	CAT	AAT	GCC	AAG	ACA	AAG	CCG	CGG
		885			894			903			912			921			930		939
Glu	Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp
GAG	CAG	TTC	AAC	AGC	ACG	TAC	CGT	GTG	GTC	AGC	GTC	CTC	ACC	GTC	CTG	CAC	CAG	GAC	TGG
		948			957			966			975			984			993		1002
Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Gly	Leu	Pro	Ser	Ser	Ile	Glu	Lys
AAC	GGC	AAG	GAG	TAC	AAG	TGC	AAG	GTC	TCC	AAC	AAA	GGC	CTC	CCG	TCC	TCC	ATC	GAG	AAA
		1011			1020			1029			1038			1047			1056		1065
Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Gln
ATC	TCC	AAA	GCC	AAA	GGG	CAG	CCC	CGA	GAG	CCA	CAG	GTG	TAC	ACC	CTG	CCC	CCA	TCC	CAG
		1074			1083			1092			1101			1110			1119		1128
Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp
GAG	ATG	ACC	AAG	AAC	CAG	GTC	AGC	CTG	ACC	TGC	CTG	GTC	AAA	GGC	TTC	TAC	CCC	AGC	GAC
		1137			1146			1155			1164			1173			1182		1191
Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val
GCC	GTG	GAG	TGG	GAG	AGC	AAT	GGG	CAG	CCG	GAG	AAC	AAC	TAC	AAG	ACC	ACG	CCT	CCC	GTG
		1200			1209			1218			1227			1236			1245		1254
Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Arg	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln
GAC	TCC	GAC	GGC	TCC	TTC	TTC	CTC	TAC	AGC	AGG	CTA	ACC	GTG	GAC	AAG	AGC	AGG	TGG	CAG
		1263			1272			1281			1290			1299			1308		1317
Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys
GGG	AAT	GTC	TTC	TCA	TGC	TCC	GTG	ATG	CAT	GAG	GCT	CTG	CAC	AAC	CAC	TAC	ACA	CAG	AAG
		1326			1335			1344			1353			1362			1371		1380
Leu	Ser	Leu	Ser	Leu	Gly	L													

8 / 32
Figure 6

Frame 1 Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp Val Leu Ser
ATG AAA CAC CTG TGG TTC TTC CTC CTC CTG GTG GCA GCC CCC AGA TGG GTC TTG TCC
9 18 27 36 45 54

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr
CAG GTG CAG CTG CAG GAG TCG GGC CCA GGA CTG GTG AAG CCT TCG GAG ACC CTG TCC CTC ACC
66 75 84 93 102 111 120

Cys Ser Val Ser Gly Gly Ser Ile Ser Gly Asp Tyr Tyr Trp Phe Trp Ile Arg Gln Ser Pro
TGC AGT GTC TCT GGT GGC TCC ATC AGC GGT GAC TAT TAT TGG TTC TGG ATC CGC CAG TCC CCA
129 138 147 156 165 174 183

Gly Lys Gly Leu Glu Trp Ile Gly Tyr Ile Tyr Gly Ser Gly Gly Gly Thr Asn Tyr Asn Pro
GGG AAG GGA CTG GAG TGG ATC GGC TAC ATA TAT GGC AGT GGT GGC ACC ACC TAC AAT CCC
192 201 210 219 228 237 246

Ser Leu Asn Asn Arg Val Ser Ile Ser Ile Asp Thr Ser Lys Asn Leu Phe Ser Leu Lys Leu
TCC CTC AAC AAT CGA GTC TCC ATT TCA ATA GAC ACG TCC AAG AAC CTC TTC TCC CTG AAA CTG
255 264 273 282 291 300 309

Arg Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Ser Asn Ile Leu Lys Tyr Leu
AGG TCT GTG ACC GCC GCG GAC ACG GCC GTC TAT TAC TGT GCG AGT AAT ATA TTG AAA TAT CTT
318 327 336 345 354 363 372

His Trp Leu Leu Tyr Trp Gly Gln Gly Val Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly
CAC TGG TTA TTA TAC TGG GGC CAG GGA GTC CTG GTC ACC GTC TCC TCA GCT AGC ACC AAG GGG
381 390 399 408 417 426 435

Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly
CCA TCC GTC TTC CCC CTG GCG CCC TGC TCC AGG AGC ACC TCC GAG AGC ACA GCC GCC CTG GGC
444 453 462 471 480 489 498

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr
TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG TCG TGG AAC TCA GGC GCC CTG ACC
507 516 525 534 543 552 561

Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val
ACC GGC GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA GGA CTC TAC TCC CTC AGC AGC GTG
570 579 588 597 606 615 624

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro
GTG ACC GTG CCC TCC AGC AGC TTG GGC ACG AAG ACC TAC ACC TGC AAC GTA GAT CAC AAG CCC
633 642 651 660 669 678 687

Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro

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9 / 32
Figure 6 (Continued)

AGC	AAC	ACC	AAG	GTG	GAC	AAG	AGA	GTT	GAG	TCC	AAA	TAT	GGT	CCC	CCA	TGC	CCA	TGC	CCA	750
		696			705			714			723			732			741			
Ala	Pro	Glu	Phe	Glu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu
GCA	CCT	GAG	TTC	GAG	GGG	GGG	CCA	TCA	GTC	TTC	CTG	TTC	CCC	CCA	AAA	CCC	AAG	GAC	ACT	CTC
		759			768			777			786			795			804			813
Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	Gln	Glu	Asp	Pro	Glu
ATG	ATC	TCC	CGG	ACC	CCT	GAG	GTC	ACG	TGC	GTG	GTG	GTG	GAC	GTG	AGC	CAG	GAA	GAC	CCC	GAG
		822			831			840			849			858			867			876
Val	Gln	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu
GTC	CAG	TTC	AAC	TGG	TAC	GTG	GAT	GGC	GTG	GAG	GTG	CAT	AAT	GCC	AAG	ACA	AAG	CCG	CGG	GAG
		885			894			903			912			921			930			939
Glu	Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu
GAG	CAG	TTC	AAC	AGC	ACG	TAC	CGT	GTG	GTC	AGC	GTC	CTC	ACC	GTC	CTG	CAC	CAG	GAC	TGG	CTG
		948			957			966			975			984			993			1002
Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Gly	Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr
AAC	GGC	AAG	GAG	TAC	AAG	TGC	AAG	GTC	TCC	AAC	AAA	GGC	CTC	CCG	TCC	TCC	ATC	GAG	AAA	ACC
		1011			1020			1029			1038			1047			1056			1065
Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Gln	Glu
ATC	TCC	AAA	GCC	AAA	GGG	CAG	CCC	CGA	GAG	CCA	CAG	GTG	TAC	ACC	CTG	CCC	CCA	TCC	CAG	GAG
		1074			1083			1092			1101			1110			1119			1128
Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile
GAG	ATG	ACC	AAG	AAC	CAG	GTC	AGC	CTG	ACC	TGC	CTG	GTC	AAA	GGC	TTC	TAC	CCC	AGC	GAC	ATC
		1137			1146			1155			1164			1173			1182			1191
Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu
GCC	GTG	GAG	TGG	GAG	AGC	AAT	GGG	CAG	CCG	GAG	AAC	AAC	TAC	AAG	ACC	ACG	CCT	CCC	GTG	CTG
		1200			1209			1218			1227			1236			1245			1254
Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Arg	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Glu
GAC	TCC	GAC	GGC	TCC	TTC	TTC	CTC	TAC	AGC	AGG	CTA	ACC	GTG	GAC	AAG	AGC	AGG	TGG	CAG	GAG
		1263			1272			1281			1290			1299			1308			1317
Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser
GGG	AAT	GTC	TTC	TCA	TGC	TCC	GTG	ATG	CAT	GAG	GCT	CTG	CAC	AAC	CAC	TAC	ACA	CAG	AAG	

Figure 7-1

Primers for the Amplification of Monkey Immunoglobulin Heavy Chain Variable Regions5' 'Sense' PrimersA. Human or Monkey heavy chain early leader sequence primers with *Sall* site

- V_H1 5' ACTAAGTCGACAT GGA^{CT}GGACCTGG 3'
- V_H2 5' ACTAAGTCGACAT GGACATACTTTGTTCCAC 3'
- V_H3 5' ACTAAGTCGACAT GGAGTTTGGGCTGAGC 3'
- V_H4 5' ACTAAGTCGACAT GAAACACCTGTGGTTCTT 3'
- V_H5 5' ACTAAGTCGACAT GGGGTCAACCGCCATCCT 3'
- V_H6 5' ACTAAGTCGACAT GTCTGTCTCCTTCCTCAT 3'

B. Human or Monkey heavy chain late leader sequence primers with *Mlu* I site

- V_H1 5' G GCA GCA GC(CT) ACG CGT GCC CAC TCC GAG GT 3' ⁺¹
- V_H2 5' G ACC GTC CCG ACG CGT GT(TC) TTG TCC CAG GT 3' ⁺¹
- V_H3 5' GCT ATT TTC ACG CGT GTC CAG TGT GAG 3' ⁺¹
- V_H4 5' GCG GCT CCC ACG CGT GTC CTG TCC CAG 3' ⁺¹
- V_H5 5' G GCT GTT CTC ACG CGT GTC TGT GCC GAG GT 3' ⁺¹

Figure 7-1 cont.

C. Human or Monkey framework 1 sequence primers with Xho I site

V_H1,3a,5 +1 CAGGTGCAGCTGGCTCGAGTCTGG

V_H2 +1 CAGGTCAACTTACTCGAGTCTGG

V_H3b +1 GAGGTGCAGCTGGCTCGAGTCTGG

V_H4 +1 CAGGTGCAGCTGGCTCGAGTCGGG

V_H6 +1 CAGGTACAGCTGGCTCGAGTCAGG

3' 'Anti-Sense' Primers.

A. Human or Monkey Heavy Chain Constant Region Primers Anti-Sense Strand with *Nhe* 1 site

IgG₁₋₄

+118
5' GGC GGA TGC GCT AGC TGA GGA GAC GG 3'
Nhe I +110

Figure 7-2

Primers for the Amplification of Monkey Immunoglobulin Light Chain Variable Regions

5' 'Sense' Primers

A. Human or Monkey kappa light chain early leader primers with *Bgl* II site

1. 5' ATCACAGATCTCTCACCATGGTGTTGCAGACCCAGGTC 3'
2. 5' ATCACAGATCTCTCACCATGG(GA)G(AT)CCCC(TA)GC(TG)CAGCT 3'
3. 5' ATCACAGATCTCTCACCATGGACATGAGGGTCCCCGCTCAG 3'
4. 5' ATCACAGATCTCTCACCATGGACAC(GAC)AGGGCCCCCACTCAG 3'

B. Human or Monkey lambda light chain early leader primers with *Bgl* II site

1. 5' ATCACAGATCTCTCACCATGGCCTGGGCTCTGCTGCTCC 3'
2. 5' ATCACAGATCTCTCACCATGGCCTGGGCTCCACTACTTC 3'
3. 5' ATCACAGATCTCTCACCATGACCTGCTCCCCTCTCCTCC 3'
4. 5' ATCACAGATCTCTCACCATGGCCTGGACTCCTCTCTTTC 3'
5. 5' ATCACAGATCTCTCACCATGACTTGGACCCCACTCCTC 3'

000720-4153T960

Figure 7-2 cont.

3' 'Anti-Sense' Primers

A. Human or Monkey kappa light chain constant region primer anti-sense strand with *Kon 1* and *BsiW1* sites

⁺¹⁰⁸
 C_{kappa} 5' CCG TTT GAT TTC CAG CTT GGT ACC TCC ACC GAA CGT 3' ⁺⁹⁷
 Kpn 1
⁺¹¹² ⁺¹⁰³
 5' TGC AGC ATC CGT ACG TTT GAT TTC CAG CTT 3'
 BsiW1

B. Human or Monkey lambda light chain constant region primer anti-sense strand with *Kpn* I, *Hind* III and *Avr* II sites

^CLambda

+107 +99
5' ACC TAG GAC GGT AAG CTT GGT ACC TCC GCC 3'
Hind III Kpn I

+107 +97
5' ACC TAG GAC GGT CA(C/G) (C/G)TT GGT ACC TCC GCC GAA CAC 3'
Kpn I

+110 +102
5' CTT GGG CTG ACC TAG GAC GGT CAG CCG 3'
Avt II

14 / 32
Figure 8

A. Heavy Chain Variable Region:

VH1	5'	CCATGGACTGGACCTGG 3'
VH2	5'	ATGGACATACTTTGTTCCAC 3'
VH3	5'	CCATGGAGTTTGGGCTGAGC 3'
VH4	5'	ATGAAACACCTGTGGTTCTT 3'
VH5	5'	ATGGGGTCAACCGCCATCCT 3'
VH6	5'	ATGTCTGTCTCCTTCCTCAT 3'

B. Heavy Chain Constant Region Anti-Sense Strand:

IgM	5'	⁺¹¹⁹ T TGG GGC GGA TGC ACT ⁺¹¹⁵ 3'
IgG ₁₋₄	5'	⁺¹¹⁹ GA TGG GCC CTT GGT GGA ⁺¹¹⁵ 3'

C. Light Chain Variable Region:

Kappa	5'	⁺⁴ G ATG ACC CAG TCT CCA (G/T)CC TC ⁺¹⁰ 3'
Lambda	5'	⁻⁹ CTC A(C/T)T (T/C)(G/A)C TGC (A/C)CA GGG TCC ⁻³ 3'

D. Light Chain Constant Region Anti-Sense Strands:

Kappa	5'	⁺¹¹⁵ AA GAC AGA TGG TGC AGC CA ⁺¹¹⁰ 3'
Lambda	5'	⁺¹¹⁸ G GAA CAG AGT GAC CGA GGG G ⁺¹¹² 3'

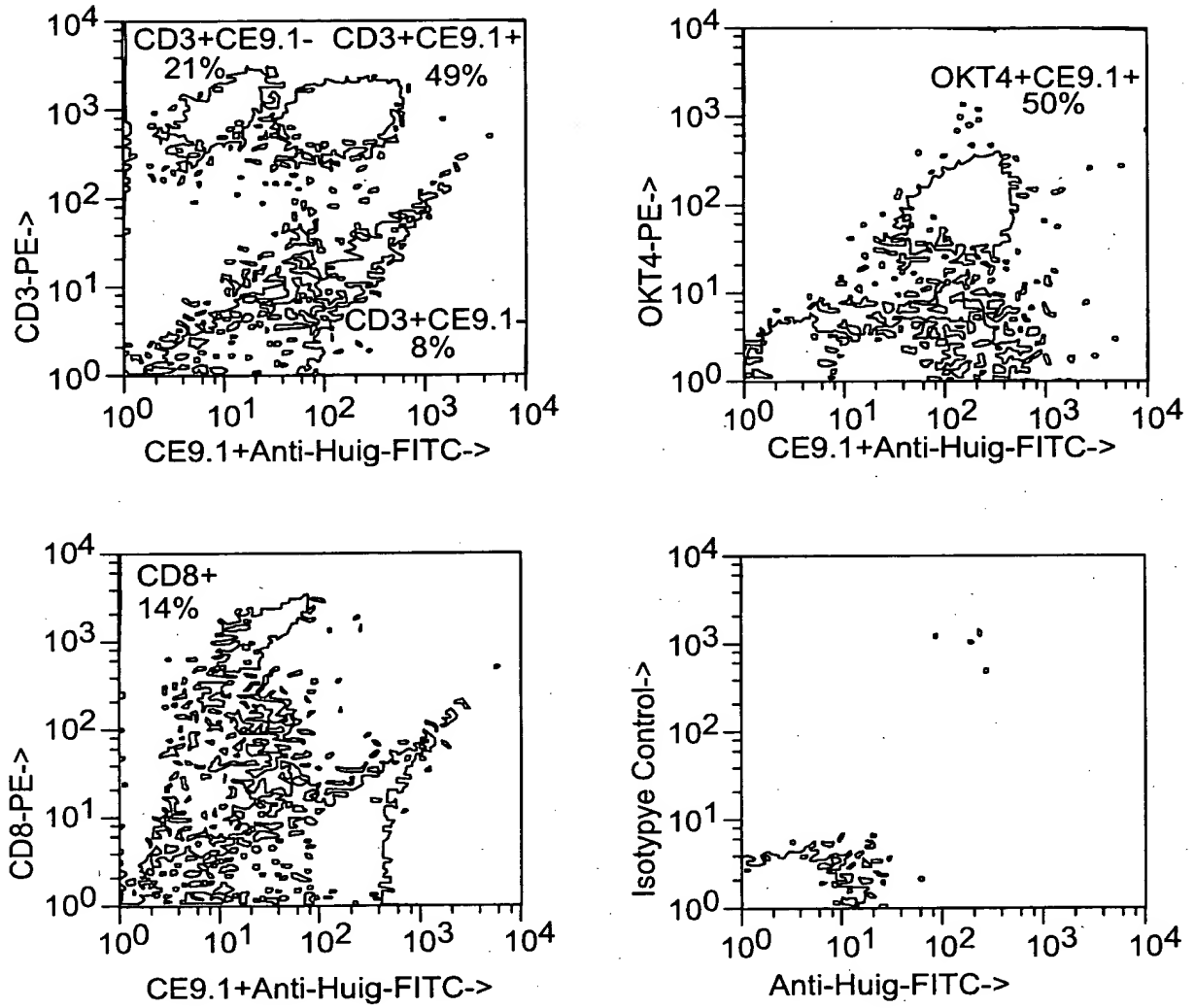


Figure 9

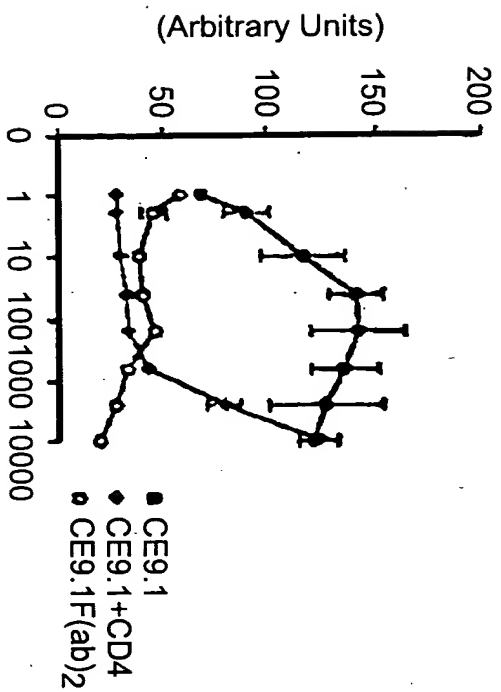


Figure 10a

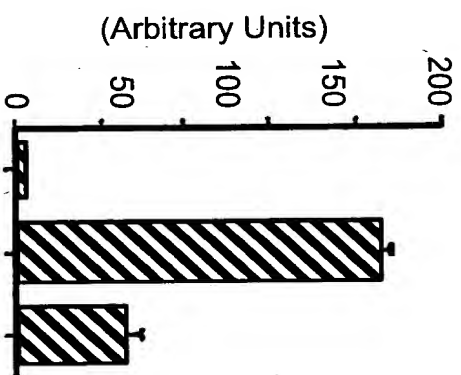


Figure 10b

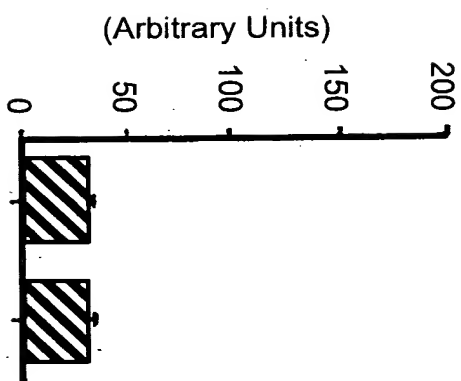


Figure 10c

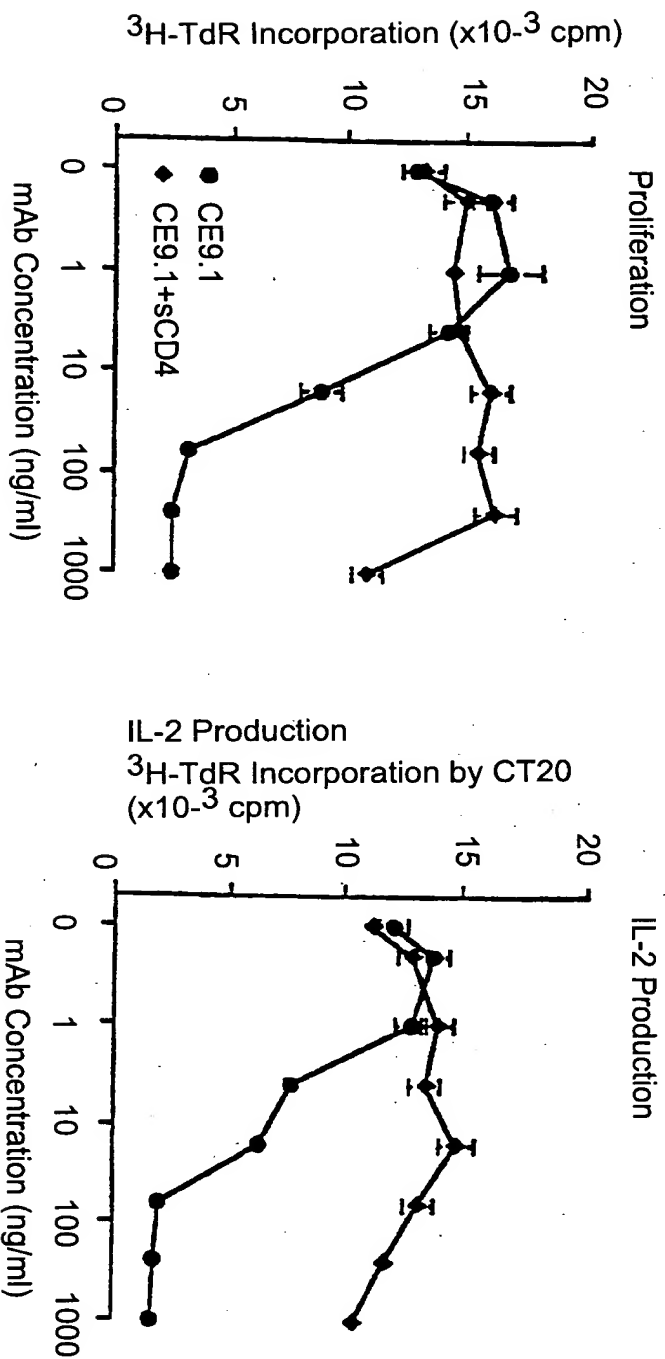


Figure 11

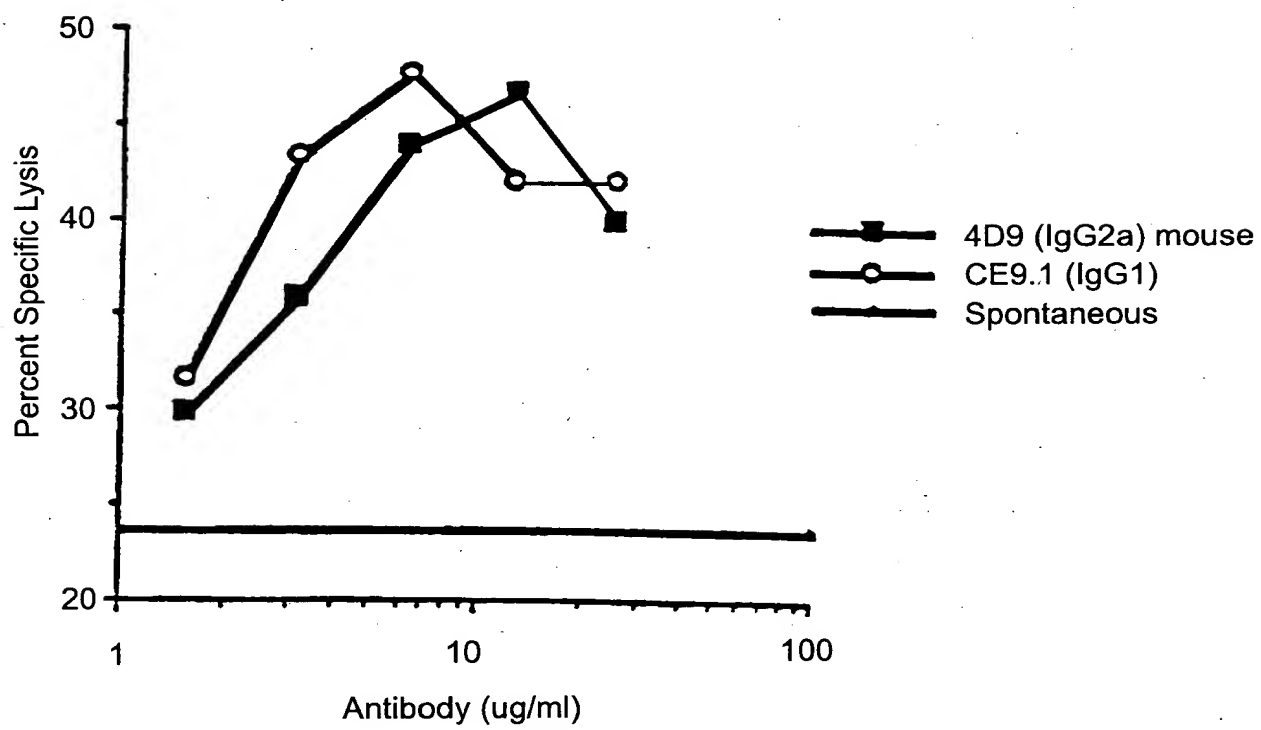


Figure 12

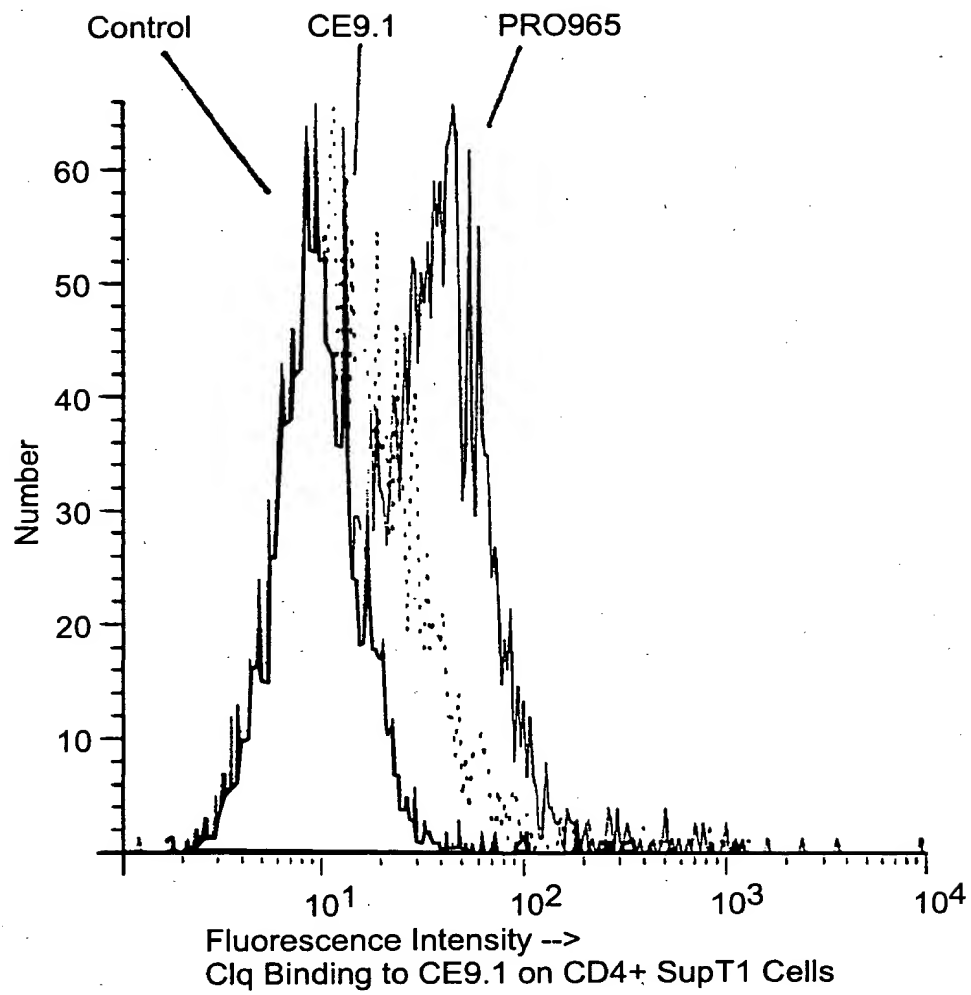


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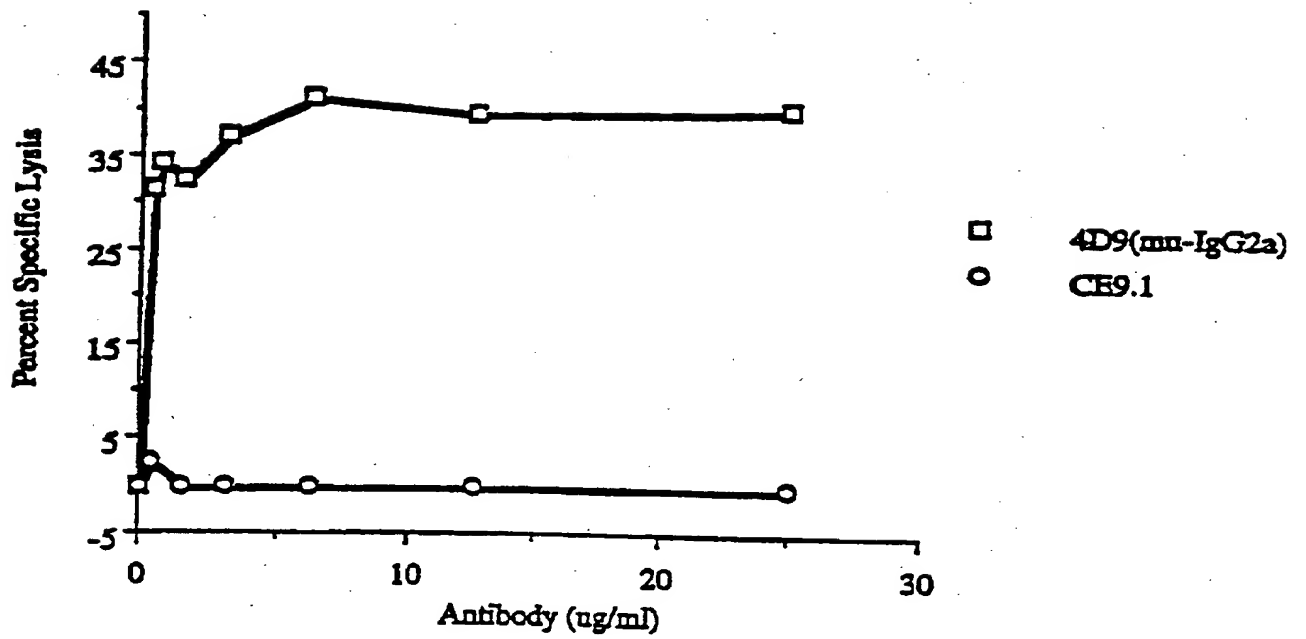


Figure 14

CD4 and CD8 Cell Counts in Chimpanzees Repeatedly Treated with 10 mpk of CE9.1

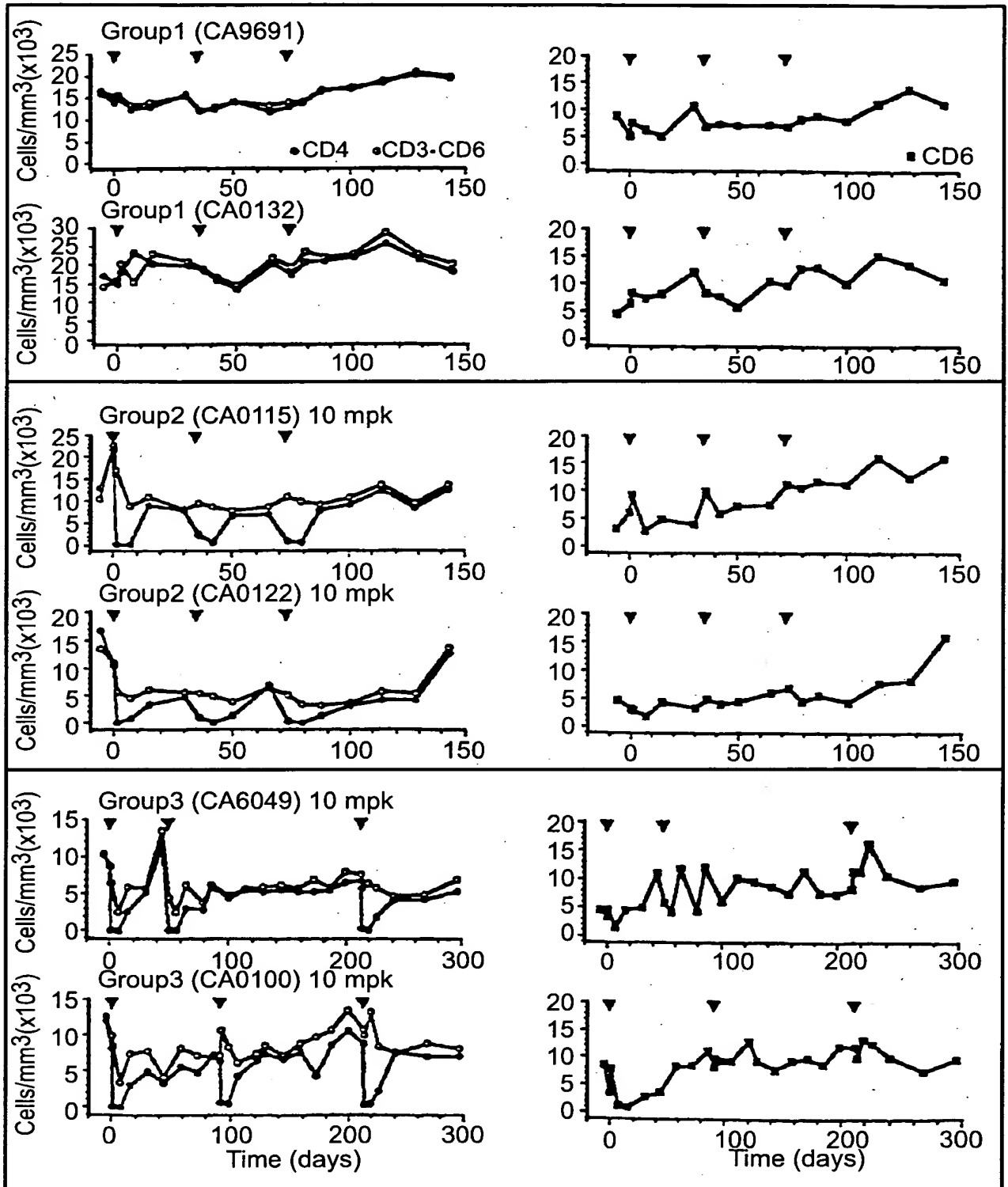


Figure 15

Figure 16

PCR Primers for Human $\gamma 4$ Constant Region

1) IDEC 462 3' PCR Primer

5' GGGG GGA TCC TCA TTT ACC CAG AGA CAG GG 3'
BamH I

2) IDEC 479 5' PCR Primer

5' GGGG GCT AGC ACC AAG GGC CCA TCC GTC TTC 3'
Nhe I

PCR Mutagenesis of Human α

3) IDEC 698 3' PCR Primer

5' CCG GGA GAT CAT GAG AGT GTC CTT GGG TTT TGG GGG GAA CAG GAA GAC
BspH I

TGA TGG TCC CCC CTC GAA CTC AGG TGC TGG GCA TGG TGG GCA TGG GGG 3'

4) Midland GE212 5' PCR Primer

Nhe I
5' TCC TCA GCT AGC ACC AAG GGG CCA TCC 3'
Destroys Apa I site

Figure 17

Frame 1 Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp Val Leu Ser
 ATG AAA CAC CTG TGG TTC TTC CTC CTC CTG GTG GCA GCC CCC AGA TGG GTC TTG TCC
 9 18 27 36 45 54

+1
 Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr
 CAG GTG CAG CTG CAG GAG TCG GGC CCA GGA CTG GTG AAG CCT TCG GAG ACC CTG TCC CTC ACC
 66 75 84 93 102 111 120

Cys Ser Val Ser Gly Gly Ser Ile Ser Gly Asp Tyr Tyr Trp Phe Trp Ile Arg Gln Ser Pro
 TGC AGT GTC TCT GGT GGC TCC ATC AGC GGT GAC TAT TAT TGG TTC TGG ATC CGC CAG TCC CCA
 129 138 147 156 165 174 183

Gly Lys Gly Leu Glu Trp Ile Gly Tyr Ile Tyr Gly Ser Gly Gly Gly Thr Asn Tyr Asn Pro
 GGG AAG GGA CTG GAG TGG ATC GGC TAC ATC TAT GGC AGT GGT GGG GGC ACC AAT TAC AAT CCC
 192 201 210 219 228 237 246

Ser Leu Asn Asn Arg Val Ser Ile Ser Ile Asp Thr Ser Lys Asn Leu Phe Ser Leu Lys Leu
 TCC CTC AAC AAT CGA GTC TCC ATT TCA ATA GAC ACG TCC AAG AAC CTC TTC TCC CTG AAA CTG
 255 264 273 282 291 300 309

Arg Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Ser Asn Ile Leu Lys Tyr Leu
 AGG TCT GTG ACC GCC GCG GAC ACG GCC GTC TAT TAC TGT GCG AGT AAT ATA TTG AAA TAT CTT
 318 327 336 345 354 363 372

His Trp Leu Leu Tyr Trp Gly Gln Gly Val Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly
 CAC TGG TTA TTA TAC TGG GGC CAG GGA GTC CTG GTC ACC GTC TCC TCA GCT AGC ACC AAG GGG
 381 390 399 408 417 426 435

000140"47627950

Figure 17 Continued

Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Cys	Ser	Arg	Ser	Thr	Ser	Glu	Ser	Thr	Ala	Ala	Leu	Gly
CCA	TCC	GTC	TTC	CCC	CTG	GCG	CCC	TGC	TCC	AGG	AGC	ACC	TCC	GAG	AGC	ACA	GCC	GCC	CTG	GCC
		444			453			462		471				480			489			498
Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr
TGC	CTG	GTC	AAG	GAC	TAC	TTC	CCC	GAA	CCG	GTG	ACG	GTG	TCC	TGG	AAC	TCA	GCC	GCC	CTG	ACC
		507			516			525			534			543			552			561
Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val
AGC	GCC	GTG	CAC	ACC	TTC	CCG	GCT	GTC	CTA	CAG	TCC	TCA	GGA	CTC	TAC	TCC	CTC	AGC	AGC	GTG
		570			579			588			597			606			615			624
Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Lys	Thr	Tyr	Thr	Cys	Asn	Val	Asp	His	Lys	Pro
GTG	ACC	GTG	CCC	TCC	AGC	TTG	GCG	ACG	AAG	ACC	TAC	ACC	TGC	AAC	GTA	GAT	CAC	AAG	CCC	CCC
		633			642			651			660			669			678			687
Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Ser	Lys	Tyr	Gly	Pro	Pro	Cys	Pro	Pro	Cys	Pro
AGC	AAC	ACC	AAG	GTG	GAC	AAG	AGA	GTT	GAG	TCC	AAA	TAT	GGT	CCC	CCA	TGC	CCA	CCA	TGC	CCA
		696			705			714			723			732			741			750
Ala	Pro	Glu	Phe	Glu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu
GCA	CCT	GAG	TTC	GAG	GGG	GGA	CCA	TCA	GTC	TTC	CTG	TTC	CCC	CCA	AAA	CCC	AAG	GAC	ACT	CTC
		759			768			777			786			795			804			813
Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	Gln	Glu	Asp	Pro	Glu
ATG	ATC	TCC	CGG	ACC	CCT	GAG	GTC	ACG	TGC	GTG	GTG	GTG	GAC	GTG	AGC	CAG	GAA	GAC	CCC	GAG
		822			831			840			849			858			867			876
Val	Gln	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu
GTG	CAG	TTC	AAC	TGG	TAC	GTG	GAT	GCG	GTG	GAG	GTG	CAT	AAT	GCC	AAG	ACA	AAG	CCG	CGG	GAG
		885			894			903			912			921			930			939
Glu	Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu
GAG	CAG	TTC	AAC	AGC	ACG	TAC	CGT	GTG	GTC	AGC	GTC	CTC	ACC	GTC	CTG	CAC	CAG	GAC	TGG	CTG
		948			957			966			975			984			993			1002
Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Gly	Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr
AAC	GCG	AAG	GAG	TAC	AAG	TGC	AAG	GTC	TCC	AAC	AAA	GCG	CTC	CCG	TCC	TCC	ATC	GAG	AAA	ACC
		1011			1020			1029			1038			1047			1056			1065
Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Gln	Glu
ATC	TCC	AAA	GCC	AAA	GGG	CAG	CCC	CGA	GAG	CCA	CAG	GTG	TAC	ACC	CTG	CCC	CCA	TCC	CAG	GAG
		1074			1083			1092			1101			1110			1119			1128
Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile
GAG	ATG	ACC	AAG	AAC	CAG	GTC	AGC	CTG	ACC	TGC	CTG	GTC	AAA	GCG	TTC	TAC	CCC	AGC	GAC	ATC
		1137			1146			1155			1164			1173			1182			1191
Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu
GCC	GTG	GAG	TGG	GAG	AGC	AAT	GGG	CAG	CCG	GAG	AAC	AAC	TAC	AAG	ACC	ACG	CCT	CCC	GTG	CTG
		1200			1209			1218			1227			1236			1245			1254
Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Arg	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Glu
GAC	TCC	GAC	GGC	TCC	TTC	TTC	CTC	TAC	AGC	AGG	CTA	ACC	GTG	GAC	AAG	AGC	AGG	TGG	CAG	GAG
		1263			1272			1281			1290			1299			1308			1317
Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser
GGG	AAT	GTC	TTC	TCA	TGC	TCC	GTG	ATG	CAT	GAG	GCT	CTG	CAC	AAC	CAC	TAC	ACA	CAG	AAG	AGC
		1326			1335			1344			1353			1362			1371			1380
Leu	Ser	Leu	Ser	Leu	Gly	Lys	TER													
CTC	TCC	CTG	TCT	CTG	GGT	AAA	TGA													
		1389			1398															

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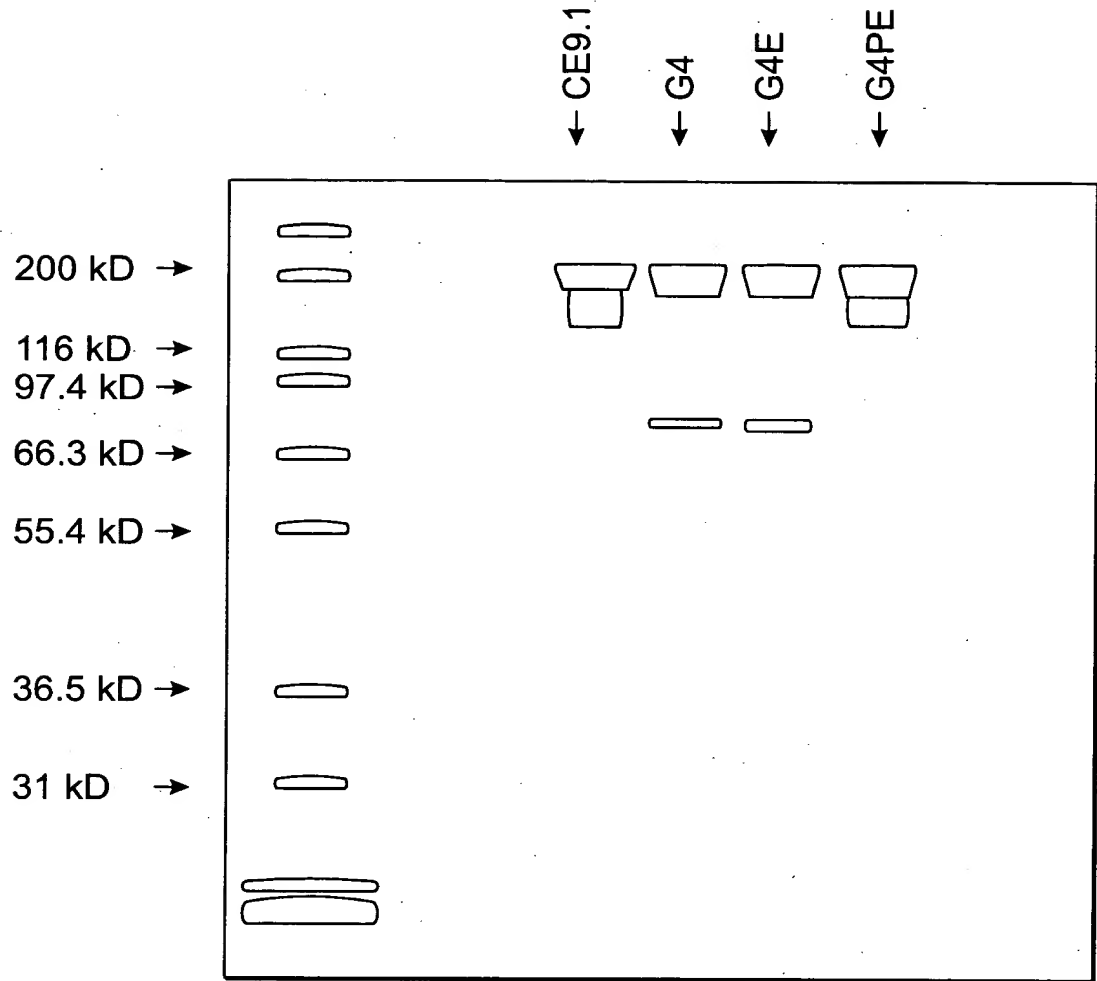


Figure 18

Figure 19

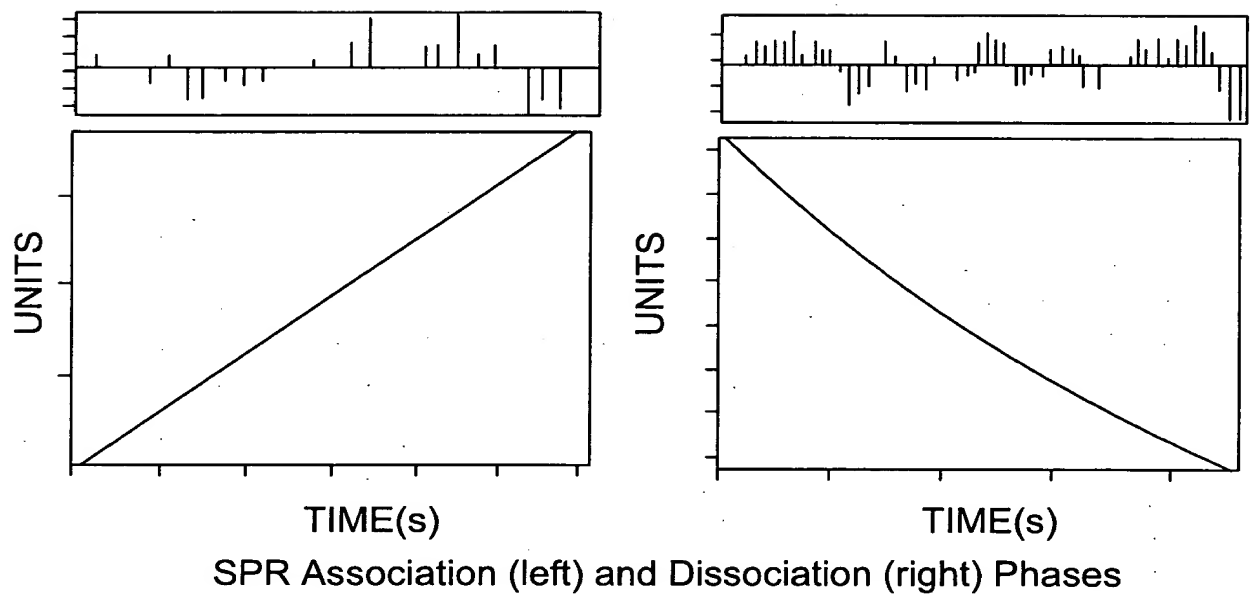


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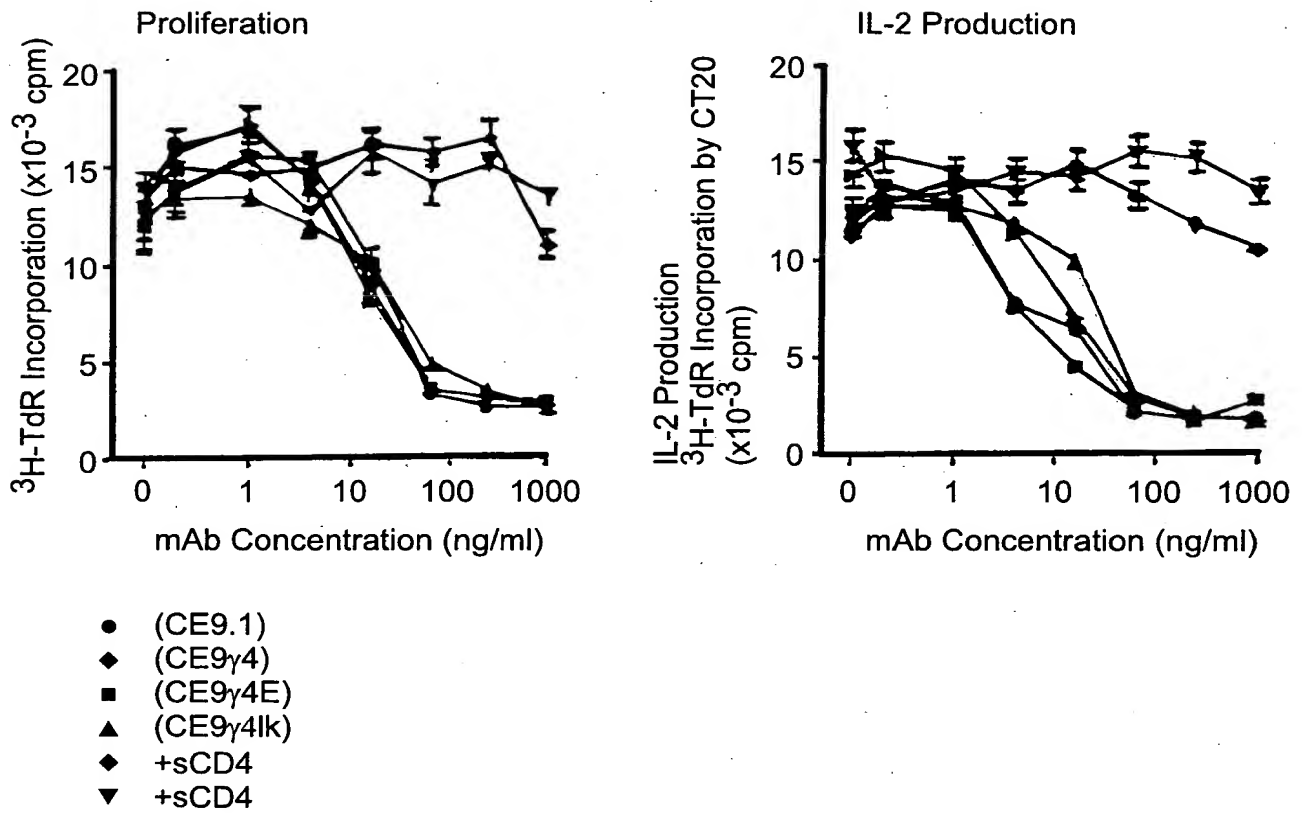


Figure 21

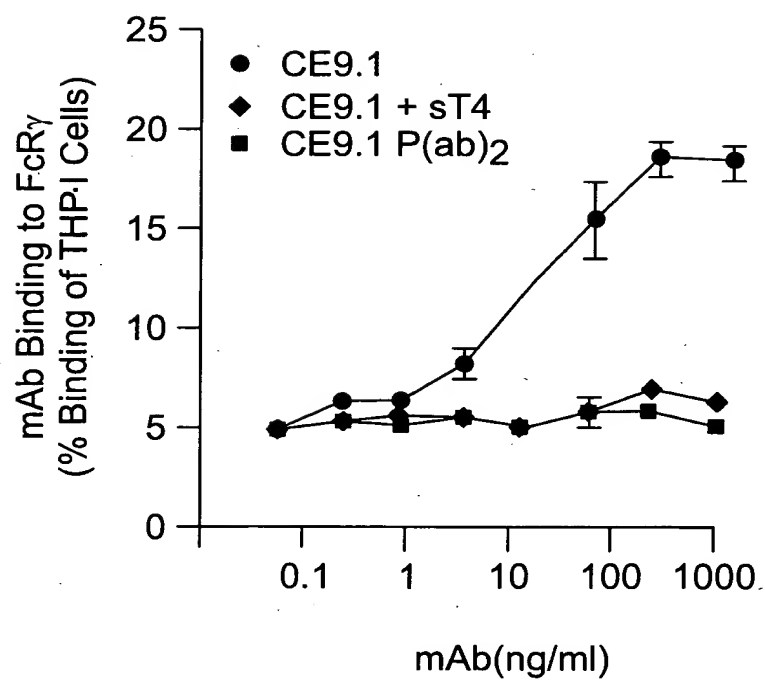
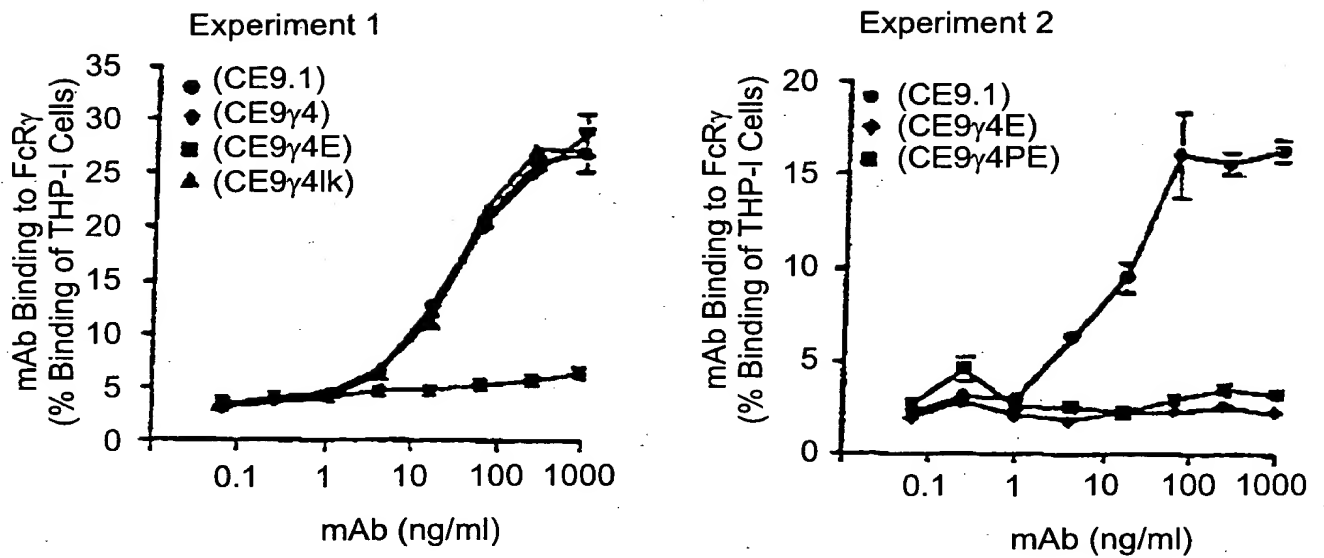


Figure 22



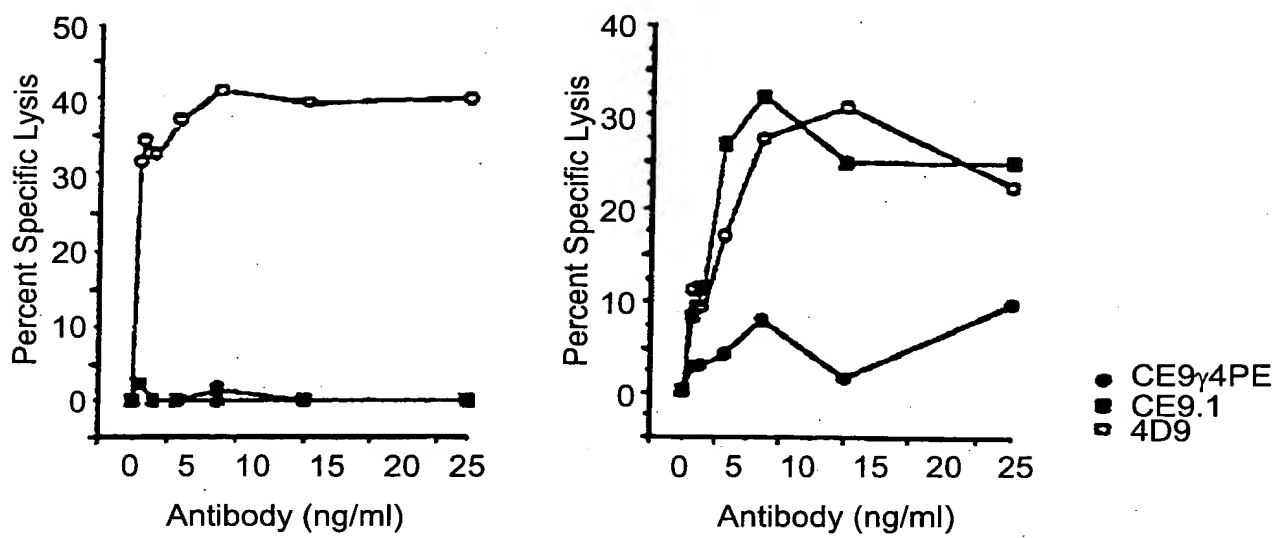
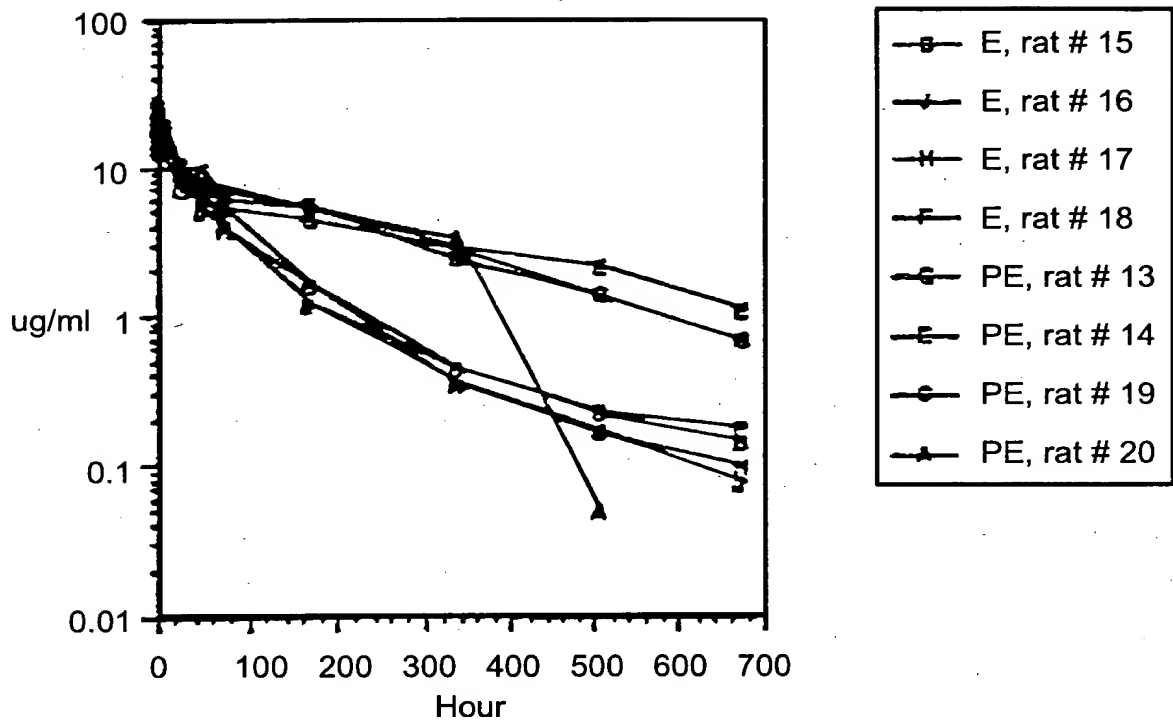


Figure 23

Figure 24



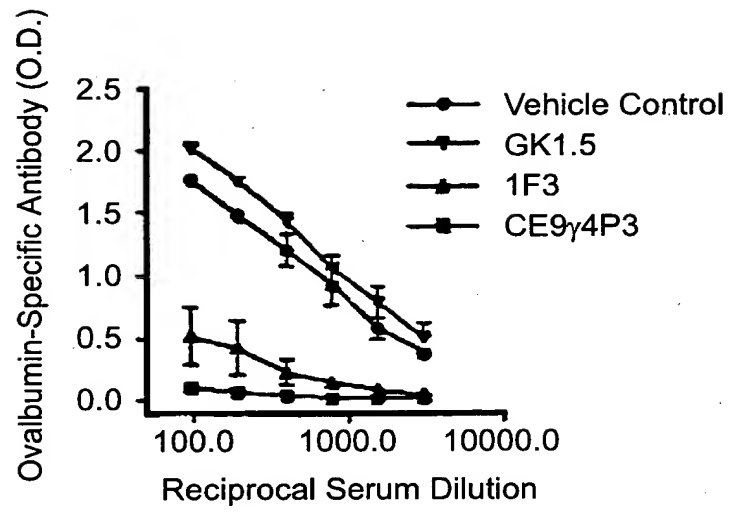


Figure 25